

SUBJECT INDEX

A

aba mutants

salt and drought stress
signal transduction,
258–59, 263–65

ABC model

rice as comparative
genomics model and,
408–9

ABF genes

salt and drought stress
signal transduction,
264–65

AB genes

cell separation processes
and, 139
salt and drought stress
signal transduction,
264–65

Abiotic stress

chlororespiration and,
540–41
lipoxygenase pathway and,
275–76, 290
plant responses to insect
herbivory and, 301

ABP gene

auxin signaling and,
377–79

Abscisic acid (ABA)

cell separation processes
and, 135, 139
nonselective cation
channels and, 76
salt and drought stress
signal transduction, 247,
258–66

Abscission

cell separation processes
and, 131–35

Acclimative response

temperature stress in higher
plants and

active oxygen species
detoxification systems,
229–30
future research, 238–39
glycinebetaine, 230–31
heat-shock proteins, 226,
228–29

introduction, 225–28

membrane lipids,
231–38
phosphatidylglycerol,
232–33
polyunsaturated fatty
acids, 234, 237–38
trienoic fatty acids,
235–37

Acer pseudoplanatus

nonselective cation
channels and, 80

Acorus spp.

vascular tissue
differentiation and pattern
formation, 185

Activase

Rubisco and, 461–65

Active oxygen species
temperature tolerance
genes and, 225, 227,
229–30

Active sites

α -ketoadic dehydrogenase
complexes and, 357
Rubisco and, 449–65

Acyl-homoserine lacton
system marine diatoms
and, 119

Ade genes

phytochelatins and
metallothioneins, 162–63

Adenosine triphosphate
(ATP)

chlororespiration and, 536,
540–41

nonselective cation

channels and, 70, 84

phytochelatins and
metallothioneins, 167
Rubisco and, 461–62

ADO2 gene

phytochrome-dependent
signaling and, 342

Aequorin

nonselective cation
channels and, 91

Aerenchyma

cell separation processes
and, 149

Aerobic soils

nitrate signaling pathways
and, 203–17

AGAMOUS gene

Arabidopsis meristem
maintenance and, 59–62
rice as comparative
genomics model and, 408

AGO gene

vascular tissue
differentiation and pattern
formation, 195–96

AGRI gene

root gravitropism and,
433–35

Agrobacterium tumefaciens
nitrate signaling pathways
and, 208

rice as comparative
genomics model and, 402

AKT channel family

nonselective cation
channels and, 88, 90

Alcaligenes eutrophus regulation of lysine metabolism in plants and, 36–37

Rubisco and, 459

Alcohols

- leaf
- lipoxygenase pathway and, 275, 281–83, 285, 287–89

Aldehydes

- lipoxygenase pathway and, 275, 281–83, 285, 287–89
- marine diatoms and, 119

ALF gene rice as comparative genomics model and, 406

Algae

- chlororespiration and, 423–42
- history of research, 6–7, 14–15, 21
- marine diatoms and, 109–25
- nonselective cation channels and, 77
- phytochelatins and metallothioneins, 172

Rubisco and, 454–55, 460, 462

Allium cepa nonselective cation channels and, 75

Allium porrum cell separation processes and, 148

Alternative oxidase chlororespiration and, 523, 533–34

Altruism marine diatoms and, 119

Amides regulation of lysine metabolism in plants and, 33–34, 39

Amino acids regulation of lysine metabolism in plants and, 27–40

α -Amino adipic acid pathway

Amino adipic semialdehyde dehydrogenase regulation of lysine metabolism in plants and, 35–39

Amyloplasts root-cap columellar root gravitropism and, 421–40

Anabaena spp. Rubisco and, 462

Anoxygenic photosynthetic organisms complex evolution of photosynthesis and, 503–25

ANR1 gene nitrate signaling pathways and, 211

ANT promoter *Arabidopsis* meristem maintenance and, 57

Antenna primary photochemistry of photosystem II and, 555–57

Anther dehiscence cell separation processes and, 145–47

Antibiotics chlororespiration and, 530, 538, 540

marine diatoms and, 121–22

Antifungal compounds lipoxygenase pathway and, 275

Antimicrobial compounds lipoxygenase pathway and, 275

Antimycin A chlororespiration and, 530, 538, 540

Antirrhinum spp.

rice as comparative genomics model and, 407

vascular tissue differentiation and pattern formation, 194

AOS gene plant responses to insect herbivory and, 310

APETALA genes *Arabidopsis* meristem maintenance and, 59

rice as comparative genomics model and, 408

AP genes rice as comparative genomics model and, 404, 407–9

Apoproteins reaction center complex evolution of photosynthesis and, 503–25

Apoptosis vascular tissue differentiation and pattern formation, 193

Arabidopsis thaliana auxin signaling and, 379–82, 384, 386–89, 392

cell separation processes and, 133, 135–42, 144–47, 150

chlororespiration and, 528, 530–32

α -ketoadic dehydrogenase complexes and, 362–63, 365–68, 370

lipoxygenase pathway and, 279, 282–84, 286–89

marine diatoms and, 116, 118, 123

nitrate signaling pathways and, 204–12, 214–17

nonselective cation channels and, 67, 71–73, 76–79, 86, 88–95

phytochelatins and

metallothioneins, 159, 161–73, 175–78
 phytochrome-dependent signaling and, 329–47
 plant responses to insect herbivory and, 309, 311, 314–17, 320
 regulation of lysine metabolism in plants and, 32–33, 35–38
 rice as comparative genomics model and, 399–413
 root gravitropism and, 423–26, 429–30, 432–33, 435–37
 Rubisco and, 462
 salt and drought stress signal transduction, 253–56, 258–59, 261–65
 shoot and floral meristem maintenance in CLV genes restrict meristem cell accumulation, 49–52
 CLV receptor complex, 52–54
 CLV signal transduction, 55–56
 conclusions, 62
 determinant vs indeterminant meristems, 49
 feedback regulation of stem cell fate, 56–59
 floral meristem organization, 47–49
 introduction, 46–47
 maintenance of shoot apical meristematic state, 49–59
 regulation of floral meristematic state, 59–62
 shoot apical meristem organization, 47–49
 temperature tolerance genes and, 227–38
 vascular tissue differentiation and pattern formation, 183, 187–92, 194–97
Archaeabacteria
 Rubisco and, 451
AREB genes
 salt and drought stress signal transduction, 264–65
ARF genes
 auxin signaling and, 377, 388–90
 root gravitropism and, 436–37
ARG/RHG gene
 root gravitropism and, 429–30
arg1 mutant
 root gravitropism and, 429–30
ARL2 gene
 root gravitropism and, 429–30
ARR gene
 nitrate signaling pathways and, 215
 phytochrome-dependent signaling and, 341
Arsenate
 history of research, 20
Arsenic
 membrane lipids and, 1
Arthrobacter globiformis
 temperature tolerance genes and, 231
Arthropods
 plant responses to insect herbivory and, 299–321
ASK genes
 phytochrome-dependent signaling and, 345
Asparagine
 regulation of lysine metabolism in plants and, 33–34
Aspartate-family pathway
 regulation of lysine metabolism in plants and, 28–32, 39
Aspergillus nidulans
 marine diatoms and, 116
 nitrate signaling pathways and, 206
Aster spp.
 nonselective cation channels and, 74, 77
AtAMT1.1 gene
 nitrate signaling pathways and, 207
AtCCH1 gene
 nonselective cation channels and, 91
AtEXP10 gene
 cell separation processes and, 138
ATHB8 gene
 vascular tissue differentiation and pattern formation, 188–91
AtHKT1 gene
 salt and drought stress signal transduction, 253, 262, 265
AtMyb gene
 salt and drought stress signal transduction, 264
AtNRT genes
 nitrate signaling pathways and, 205–12
AtPCS genes
 phytocalelatins and metallothioneins, 161–62, 166–67
AtPLC1 gene
 salt and drought stress signal transduction, 256
AtSUC3 gene
 cell separation processes and, 145
Auxins
 Aux/IAA protein family, 382–92

auxin binding protein 1, 378–79
 auxin response factors, 388–90
 cell separation processes and, 135
 conclusions, 392
 dimerization, 388–90
 gene expression model, 390–92
 introduction, 378
 nitrate signaling pathways and, 203, 212–14, 217
 perception, 378–80
 phytochrome-dependent signaling and, 340
 root gravitropism and, 421, 430–39
RUB1, 385–88
SCF^{TIR1}, 382–88
 signal transduction, 380–92
 ubiquitin-mediated protein degradation, 380–82
 vascular tissue differentiation and pattern formation, 183–97

avb1 mutant
 vascular tissue differentiation and pattern formation, 194–95

AXR genes
 auxin signaling and, 380–81, 383–84, 386–88
 nitrate signaling pathways and, 211
 vascular tissue differentiation and pattern formation, 191, 196

Azotobacter vinelandii
 complex evolution of photosynthesis and, 510
 α -ketoacid dehydrogenase complexes and, 368–69

B
Bacillus stearothermophilus
 α -ketoacid dehydrogenase complexes and, 368–69
Bacillus subtilis
 α -ketoacid dehydrogenase complexes and, 362

Bacteria
 chlororespiration and, 423–42
 complex evolution of photosynthesis and, 503–25
 history of research, 14
 α -ketoacid dehydrogenase complexes and, 362–64
 marine diatoms and, 117–19
 nonselective cation channels and, 85, 91–92
 phytochelatins and metallothioneins, 166, 174
 primary photochemistry of photosystem II and, 551, 557–58
 regulation of lysine metabolism in plants and, 30–32, 34–36, 39
 Rubisco and, 451, 454–55, 457, 459, 462
 targeted mutagenesis in *Physcomitrella patens* and, 477
 temperature tolerance genes and, 226, 229–31, 233–34

bdl mutant
 vascular tissue differentiation and pattern formation, 196

Bemisia tabaci
 plant responses to insect herbivory and, 304

Benson AA, 1–23

Beta vulgaris
 nonselective cation channels and, 81–82

BGL2 gene
 plant responses to insect herbivory and, 312

herbivory and, 312
 Bioinorganic pattern formation
 marine diatoms and, 109

Biotechnology
 cell separation processes and, 131
 phytochelatins and metallothioneins, 178

Bloom decline
 marine diatoms and, 119

Boas F
 history of research, 19–20

bodenlos mutant
 vascular tissue differentiation and pattern formation, 191

Bolidomonas spp.
 marine diatoms and, 121

Boltzmann equation
 primary photochemistry of photosystem II and, 562

Borohydride
 primary photochemistry of photosystem II and, 560

Botryococcus braunii
 history of research, 21

Botrytis cinerea
 plant responses to insect herbivory and, 311

Branched-chain α -ketoacid dehydrogenase complex
 α -ketoacid dehydrogenase complexes and, 365–66

Branching root
 nitrate signaling pathways and, 212–14

Brassica napus
 cell separation processes and, 134, 136, 140, 142–45
 phytochelatins and metallothioneins, 171, 175
 plant responses to insect herbivory and, 316

Brassica spp.
phytochelatins and
metallothioneins, 162,
164, 170–71

BRII gene
rice as comparative
genomics model and, 410

Brown algae
phytochelatins and
metallothioneins, 172

Bryonia dioica
nonselective cation
channels and, 85

C

Ca^{2+}
 α -ketoacid dehydrogenase
complexes and, 362
nonselective cation
channels and, 69, 71–72,
76–85, 87, 89–93, 95–96
phytochrome-dependent
signaling and, 333, 335,
344–45
regulation of lysine
metabolism in plants and,
32, 37
root gravitropism and,
427–29, 431, 434, 438
salt and drought stress
signal transduction, 247,
250–52, 256–58, 260, 262

CAB genes
marine diatoms and, 114
phytochelatins and
metallothioneins, 161–62,
166–67
phytochrome-dependent
signaling and, 340

Cadmium
phytochelatins and
metallothioneins, 163,
166–70, 174–78

Caenorhabditis elegans
 α -ketoacid dehydrogenase
complexes and, 368–69
phytochelatins and
metallothioneins, 163,
167, 169–70

Caenorhabditis briggsae
phytochelatins and
metallothioneins, 163

Cafeteria roenbergensis
marine diatoms and, 120

CAL gene
rice as comparative
genomics model and, 404

Calanus plumchrus
history of research, 18–19

Calmodulin
phytochrome-dependent
signaling and, 344–45

Cambium
vascular tissue
differentiation and pattern
formation, 188–90

Candida glabrata
phytochelatins and
metallothioneins, 168

Capsicum annuum
lipoxygenase pathway and,
282–83

Car^+
primary photochemistry of
photosystem II and, 569,
571

Carbon
chlororespiration and,
537–38
history of research, 1–23
Rubisco and, 449–65

Carbon dioxide (CO_2)
history of research, 1–23
Rubisco and, 449–65

Carotenoid biosynthesis
genes
complex evolution of
photosynthesis and,
517–18

Carotenoids
marine diatoms and,
120–21

Casein kinase II
regulation of lysine
metabolism in plants and,
37–38

Catabolism
regulation of lysine
metabolism in plants and,
27–28, 34–39

Catharanthus roseus
plant responses to insect
herbivory and, 321

Cation channels
nonselective, 67–96

CBF genes
salt and drought stress
signal transduction,
264–65

CCA gene
phytochrome-dependent
signaling and, 341, 346

CDC53 gene
auxin signaling and, 380

Cell differentiation
vascular tissue
differentiation and pattern
formation, 183–97

Cell division
marine diatoms and,
112–13

Cell membrane model
history of research, 17–18

Cell separation processes
abscission
anatomical changes,
135–36
biochemical changes,
136–39
expansin, 138
 β -1,4-glucanase, 136–37
manipulation of process,
147–48
miscellaneous genes and
proteins, 139
molecular changes,
136–39
morphogenesis of
abscission zone,
132–34
pathogenesis-related

proteins, 139
 polygalacturonase, 137–38
 regulation of timing, 134–35
 secondary abscission zones, 133–34
 fruit, 150
 future research, 150
 introduction, 131
 leaves, 149
 overview, 131–32
 pod dehiscence, 140–41
 anther dehiscence, 145–47
 biochemical changes, 143–45
 breeding of plants resistant to dehiscence, 145
 β -1,4-glucanase, 143
 manipulation of process, 147–48
 miscellaneous genes and proteins, 144–45
 molecular changes, 143–45
 morphogenesis of pod dehiscence zone, 141
 polygalacturonase, 143–44
 regulation of timing, 142–43
 roots, 148–49
 seeds, 148
 stems, 149

Cell wall
 degradation
 cell separation processes and, 131–50
 marine diatoms and, 109–25

Cell-to-cell adhesion
 cell separation processes and, 131

Cellular response
 plant responses to insect

herbivory and, 299
CEN gene
 rice as comparative genomics model and, 407
CePcS1 gene
 phytocelatins and metallothioneins, 163
Chaperones
 regulation of lysine metabolism in plants and, 30–31
Chara spp.
 root gravitropism and, 427
Chenopodium rubrum
 nonselective cation channels and, 81
Chironomus spp.
 phytocelatins and metallothioneins, 163
CHL1 gene
 nitrate signaling pathways and, 205, 212
Chlamydomonas reinhardtii
 chlororespiration and, 525–28, 530–36, 539
 marine diatoms and, 118, 122
 primary photochemistry of photosystem II and, 569
 Rubisco and, 454–56, 458–60, 463–64
 salt and drought stress signal transduction, 258

Chlorella spp.
 history of research, 5–7, 16, 21
 chlororespiration and, 528
 marine diatoms and, 122

Chlorins
 primary photochemistry of photosystem II and, 556, 559–61

Chlorobium tepidum
 complex evolution of photosynthesis and, 510, 514

Chloroflexus aurantiacus

complex evolution of photosynthesis and, 510, 514
Chlorophylls
 marine diatoms and, 119–20
 primary photochemistry of photosystem II and, 551–62, 564, 568–69

Chloroplasts
 chlororespiration and, 523–42
 lipoxygenase pathway and, 278–79, 285
 marine diatoms and, 118
 Rubisco and, 449–65

Chlororespiration
 abiotic stress responses, 540–41
 activity, 534–35, 536
 chloroplast biogenesis, 538
 chlororespiratory electron carriers, 537–41
 conclusions, 541–42
 current model, 534–37
 cyclic electron transfer around photosystem I, 539–40
 electrogenicity, 536
 interactions between photosynthesis and respiration, 525–27
 introduction, 524–25
 mitochondrial respiration, 537
 nonphotochemical oxidation of plastoquinones, 532–34
 nonphotochemical reduction of plastoquinones, 527–28
 nonphotosynthetic plastids, 538
 perspectives, 541–42
 photosynthesis, 537
 plastid carbon metabolism in the dark, 537–38

plastid-encoded *Ndh* complex homologous to complex I, 528–29

posttranscriptional regulation, 538–39

PQ-oxidase, 533–34

PQ-reductase, 530–32

reverse electron flow through *Ndh* complex, 532–33

transcriptional regulation, 538–39

Choline phosphate history of research, 15

Chodny-Went theory root gravitropism and, 437–38

Chrysomela populi plant responses to insect herbivory and, 314

Circadian rhythm chlororespiration and, 537–38

phytochrome-dependent signaling and, 329–47

Cl^- nonselective cation channels and, 71–72, 83

Cladosporium fulvum nonselective cation channels and, 77

CLAVATA genes *Arabidopsis* meristem maintenance and, 45, 49–62

CLE gene *Arabidopsis* meristem maintenance and, 51–52

Clivia spp. nonselective cation channels and, 75, 78

CNGC genes nonselective cation channels and, 88–89

CodA gene temperature tolerance genes and, 231

Coevolution plant responses to insect herbivory and, 302

coil mutant cell separation processes and, 146–47

Coleus spp. vascular tissue differentiation and pattern formation, 186

Community-level response plant responses to insect herbivory and, 299

Comparative genomics rice as comparative genomics model and, 399–413

Compartmentalization regulation of lysine metabolism in plants and, 27

Compatible solutes temperature tolerance genes and, 225, 227, 230–31

Competitive inhibition Rubisco and, 449–65

Complex evolution photosynthesis and, 503–25

Complexity plant responses to insect herbivory and, 320–21

COP/DET/FUS pathway phytochrome-dependent signaling and, 340–45

COR genes salt and drought stress signal transduction, 261–63, 265

Costs of defense plant responses to insect herbivory and, 302–3

Cotesia marginiventris plant responses to insect herbivory and, 318

Craterostigma plantagineum

salt and drought stress signal transduction, 258

CRE1 gene vascular tissue differentiation and pattern formation, 189

Cre/lox-mediated site-specific recombination

complex evolution of photosynthesis and, 492–94

Cryptochromes phytochrome-dependent signaling and, 329–47

Cs^+ nonselective cation channels and, 76–77, 83–84, 96

Cucumis spp. lipoxygenase pathway and, 282–83

Cucurbita spp. nitrate signaling pathways and, 208

phytochrome-dependent signaling and, 332

Cullin gene families auxin signaling and, 380–81

Curvature response root gravitropism and, 421–40

cvp mutants vascular tissue differentiation and pattern formation, 196

Cyanidium caldarium α -ketoacid dehydrogenase complexes and, 368–69

Cyanobacteria complex evolution of photosynthesis and, 503–25

marine diatoms and, 117

nonselective cation channels and, 92

Rubisco and, 454, 462

temperature tolerance
genes and, 234

Cyanophora paradoxa
complex evolution of
photosynthesis and, 514

Cyclic electron transfer
chlororespiration and,
539–40

Cyclic nucleotide-gated ion
channels (CNGCs)
nonselective cation
channels and, 67, 78–79,
87–90
salt and drought stress
signal transduction, 253

Cyclin-dependent kinases
salt and drought stress
signal transduction, 250

Cyclins
nitrate signaling pathways
and, 214

Cyclotella cryptica
marine diatoms and, 122,
125

Cylindrotheca spp.
marine diatoms and,
112–13, 116–17,
123–24
Rubisco and, 457, 460

CYP genes
lipoxygenase pathway and,
275, 283–86
plant responses to insect
herbivory and, 315

Cytochrome *b*
complex evolution of
photosynthesis and,
503–25

Cytokinins
nitrate signaling pathways
and, 203, 214–17
vascular tissue
differentiation and pattern
formation, 183–97

Cytoplasm
phytochrome-dependent
signaling and, 335–39

Cytosol
phytochrome-dependent
signaling and, 329–47
root gravitropism and,
428–29

D

Damage control and repair
salt and drought stress
signal transduction,
247–67

DapA gene
regulation of lysine
metabolism in plants and,
30

Dark
chlororespiration and,
537–38

Dasineura brassicae
cell separation processes
and, 142

"Day/night" cycles
regulation of lysine
metabolism in plants and,
34

defl mutant
cell separation processes
and, 147

Defense signaling
marine diatoms and, 119
rice as comparative
genomics model and, 399,
409–13

Defense strategies
plant responses to insect
herbivory and, 299–321

DEFICIENS transcription
factor
Arabidopsis meristem
maintenance and, 62

Dehiscence
cell separation processes
and, 131, 140–43

delayed dehiscence1 gene
cell separation processes
and, 146

Depolarization-activated

NSCCs
nonselective cation
channels and, 72

Destruction
phytochrome-dependent
signaling and, 329–47

Determinant meristems
Arabidopsis meristem
maintenance and, 49

Detoxification
heavy metal, 159–78
salt and drought stress
signal transduction,
247–67
temperature tolerance
genes and, 225, 227,
229–30

Development
auxin signaling and,
377–92
lipoxygenase pathway and,
275, 289
nitrate signaling pathways
and, 209–15
regulation of lysine
metabolism in plants and,
27, 32–36
rice as comparative
genomics model and, 399,
402–9

Diatoms
marine, 109–25

Dictyostelium discoideum
phytochelatins and
metallothioneins, 163–65

Diethylpyrocarbonate
(DEPC)
nonselective cation
channels and, 70

Differential regulation
phytochrome-dependent
signaling and, 329–47

Dihydrolipoyl acyltransferase
 α -ketoadic dehydrogenase
complexes and, 357

Dihydrolipoyl dehydrogenase
 α -ketoadic dehydrogenase

complexes and, 357

Dihydropicolinate synthase (DHPs)
regulation of lysine metabolism in plants and, 28–36, 39

Dimerization
auxin signaling and, 388–90, 392

Direct defenses
plant responses to insect herbivory and, 299, 301, 303, 313–16

Disease resistance
rice as comparative genomics model and, 409–10

Ditylum brightwellii
marine diatoms and, 118

Diturnal cycle
chlororespiration and, 537–38

nitrate signaling pathways and, 209–10

Divinyl ethers
lipoxygenase pathway and, 275–76, 281–83, 285, 287–89

dnd1 mutant
nonselective cation channels and, 90

Donor-side secondary electron transfer
primary photochemistry of photosystem II and, 566–67

Downstream stress tolerance
effector genes
salt and drought stress
signal transduction, 247, 261–67

Dracaena spp.
vascular tissue
differentiation and pattern formation, 185

DREB genes
salt and drought stress

signal transduction, 264–65

Drosophila melanogaster
 α -ketoad dehydrogenase complexes and, 368–69
phytochelatins and metallothioneins, 165

Drought stress
signal transduction and, 247–67

Dynamic solvation model
primary photochemistry of photosystem II and, 566

E

Ecophysiology success
marine diatoms and, 109–25

ecrl mutant
auxin signaling and, 381

Effector genes
salt and drought stress
signal transduction, 247, 250, 261–67

Efflux carrier complexes
root gravitropism and, 432–34

ehy mutant
vascular tissue
differentiation and pattern formation, 196

EID1 gene
phytochrome-dependent signaling and, 342, 345

Electrogenicity
chlororespiration and, 536

Electron microscopy
primary photochemistry of photosystem II and, 551–71

Electron nuclear double resonance (ENDOR)
primary photochemistry of photosystem II and, 562

Electron transfer
primary photochemistry of

photosystem II and, 551, 566–67

Electron transport chain
respiratory
chlororespiration and, 423–42

Electrophysiology
nonselective cation channels and, 67–96

Electrostatics
primary photochemistry of photosystem II and, 567–68

ELF3 gene
phytochrome-dependent signaling and, 342

elil mutant
vascular tissue
differentiation and pattern formation, 191

Elicitors
insect
plant responses to insect herbivory and, 299, 301, 304–8

Elongation
nitrate signaling pathways and, 209–11
root gravitropism and, 421–40
vascular tissue
differentiation and pattern formation, 192

enb gene
cell separation processes and, 140

Endomembranes
nonselective cation channels and, 67, 72–85

Endoplasmic reticulum
nonselective cation channels and, 85

Energy transfer
primary photochemistry of photosystem II and, 555–57

Environmental signals

regulation of lysine metabolism in plants and, 32–33

Environmental stress temperature tolerance genes and, 225–39

Epifagus virginia chlororespiration and, 528

Episomal replicative transformation complex evolution of photosynthesis and, 482–84

erecta ecotype plant responses to insect herbivory and, 316

Erythrosine nonselective cation channels and, 85

Escherichia coli chlororespiration and, 533 history of research, 16 α -ketoacid dehydrogenase complexes and, 363–64, 366, 368–69 nonselective cation channels and, 85 phytochelatins and metallothioneins, 166, 174 regulation of lysine metabolism in plants and, 30 Rubisco and, 455, 457, 459, 462 temperature tolerance genes and, 229–31, 233

ESR proteins *Arabidopsis* meristem maintenance and, 51–52

Esential amino acids regulation of lysine metabolism in plants and, 27–40

Ethylene cell separation processes and, 131, 134–35, 138

plant responses to insect herbivory and, 305–6, 311

Etr1 gene cell separation processes and, 135, 142

Euglena gracilis chlororespiration and, 528

Eukaryotes marine diatoms and, 109–25

Evolution complex evolution of photosynthesis and, 503–25 α -ketoacid dehydrogenase complexes and, 357, 368–70 rice as comparative genomics model and, 399–413

Evolutionary hotspot nonselective cation channels and, 95

Expanin cell separation processes and, 138

Expressed sequence tags (ESTs) marine diatoms and, 117, 121, 123 phytochelatins and metallothioneins, 174 regulation of lysine metabolism in plants and, 37–38 rice as comparative genomics model and, 401

Extralfloral nectar plant responses to insect herbivory and, 319

F

fab1 mutant temperature tolerance genes and, 233

fad mutant cell separation processes and, 146–47

temperature tolerance genes and, 234–38

FAR1 gene phytochrome-dependent signaling and, 342

FAS genes *Arabidopsis* meristem maintenance and, 57

fass mutant vascular tissue differentiation and pattern formation, 189

Fast-activating NSCCs nonselective cation channels and, 83–84

Fast dark reversion phytochrome-dependent signaling and, 329–47

Fatty acids lipoxygenase pathway and, 275–89 temperature tolerance genes and, 234–38

FCP genes marine diatoms and, 114–15, 118

Feedback regulation *Arabidopsis* meristem maintenance and, 45, 56–59 nitrate signaling pathways and, 207–8 regulation of lysine metabolism in plants and, 28–31

fil-5 mutant vascular tissue differentiation and pattern formation, 196

FIN219 gene phytochrome-dependent signaling and, 342

Fitness-based evaluations of resistance traits plant responses to insect herbivory and, 302

FKBP12 molecular chaperone regulation of lysine metabolism in plants and, 30–31

Flavonoids regulation of lysine metabolism in plants and, 32

FLO gene rice as comparative genomics model and, 406

Floral meristem *Arabidopsis* meristem maintenance and, 45–62

Floral organ development genes rice as comparative genomics model and, 408–9

FLS2 gene rice as comparative genomics model and, 410

Fountain model of auxin transport root gravitropism and, 431–32

Fourier transform infrared spectroscopy (FTIR) primary photochemistry of photosystem II and, 558, 562

Fraction I protein history of research, 13–14

Fruit cell separation processes and, 131–50

Frustulins marine diatoms and, 112–13

fry1 mutant salt and drought stress signal transduction, 257–58, 265–66

Fucosanthin marine diatoms and, 120–21

Fucus vesiculosus phytochelatins and metallothioneins, 172, 174, 176

FUL gene cell separation processes and, 141

Functional genomics targeted mutagenesis in *Physcomitrella patens* and, 477–95

Fungi auxin signaling and, 381 lipoxygenase pathway and, 275 marine diatoms and, 120 nitrate signaling pathways and, 206 nonselective cation channels and, 77 phytochelatins and metallothioneins, 163, 173

fzp mutant rice as comparative genomics model and, 405

G

Galdieria partita Rubisco and, 454, 461

Gd³⁺ nonselective cation channels and, 79

Gene-tagged lines rice as comparative genomics model and, 401

Gene targeting targeted mutagenesis in *Physcomitrella patens* and, 477–95

Genetic engineering α -ketoacid dehydrogenase complexes and, 357 salt and drought stress signal transduction, 267 temperature tolerance genes and, 225–26

Genomics chlororespiration and, 531–34 α -ketoacid dehydrogenase complexes and, 357, 366–67 marine diatoms and, 109, 122–25 nitrate signaling pathways and, 206 nonselective cation channels and, 67, 71–73, 76–79, 86, 88–95 phytochelatins and metallothioneins, 159, 161–73, 175–78 rice as comparative genomics model and, 399–413 salt and drought stress signal transduction, 260 targeted mutagenesis in *Physcomitrella patens* and, 477–95

Geochemical evidence complex evolution of photosynthesis and, 505–7

GIGANTEA gene phytochrome-dependent signaling and, 342

GLB1 gene nitrate signaling pathways and, 209

Global warming temperature tolerance genes and, 225–26

β -1,4-Glucanase cell separation processes and, 136–37, 143

Gluconacetobacter diazotrophicus complex evolution of photosynthesis and, 510

glut1 gene marine diatoms and, 122

Glutamate

nonselective cation channels and, 67, 69, 71, 75, 79, 86, 91–93, 96 regulation of lysine metabolism in plants and, 27, 29, 35–36, 38–39

Glycinebetaine temperature tolerance genes and, 225, 227, 230–31

GNOM gene vascular tissue differentiation and pattern formation, 189

GORK channel family nonselective cation channels and, 87, 90

G proteins phytochrome-dependent signaling and, 344 rice as comparative genomics model and, 411–12

Grasses rice as comparative genomics model and, 404–8

Gravitropism root, 421–40

Green algae chlororespiration and, 534, 540 marine diatoms and, 118, 120–22 Rubisco and, 454–55, 460, 462

Green fluorescent protein (GFP) cell separation processes and, 137 marine diatoms and, 122 phytochrome-dependent signaling and, 335–39

GroE molecular chaperone regulation of lysine metabolism in plants and, 30–31

Growth auxin signaling and, 377–92 nitrate signaling pathways and, 209–15 regulation of lysine metabolism in plants and, 27 salt and drought stress signal transduction, 247–67

Gsh genes phytochelatins and metallothioneins, 162

Guillardia theca marine diatoms and, 120

GUS reporter gene cell separation processes and, 137, 139 marine diatoms and, 124 phytochrome-dependent signaling and, 335–36 regulation of lysine metabolism in plants and, 33 root gravitropism and, 434

H

H⁺ nonselective cation channels and, 84 salt and drought stress signal transduction, 250–52, 261

Haemanthus spp. nonselective cation channels and, 75, 78

HAESA gene cell separation processes and, 139

HATs nitrate signaling pathways and, 205, 209

Hd genes rice as comparative genomics model and, 403

Heat-shock proteins

temperature tolerance genes and, 225–26, 228–29

Heavy metal detoxification phytochelatins and metallothioneins in, 159–78

Helicoverpa zea plant responses to insect herbivory and, 304

Heliobacillus mobilis complex evolution of photosynthesis and, 510, 514

hem2 mutant phytochelatins and metallothioneins, 163, 168

Herbivore attack plant responses to insect herbivory and, 299–321

Heterologous conditional promoters complex evolution of photosynthesis and, 490–92

Heterotrimeric G protein rice as comparative genomics model and, 411–12

HFR1/RSF1/REP1 gene group phytochrome-dependent signaling and, 342–43

High-energy phosphate bond history of research, 6

Higher plants temperature tolerance genes and, 225–39

Histidine kinases phytochrome-dependent signaling and, 341 salt and drought stress signal transduction, 253, 265

hlg2 mutant phytochrome-dependent

signaling and, 336

Hmt genes

- phytochelatins and metallothioneins, 162–63, 167–68

Holoproteins

- reaction center
- complex evolution of photosynthesis and, 503

Homeostasis

- phytochelatins and metallothioneins in, 159–78

Homeostasis signaling pathways

- salt and drought stress
- signal transduction, 247–67

Homo sapiens

- α -ketoacid dehydrogenase complexes and, 368–69

Homologous recombination

- targeted mutagenesis in *Physcomitrella patens* and, 477–95

Homoserine dehydrogenase regulation of lysine metabolism in plants and, 29–31, 33

Hordeum vulgare

- lipoxygenase pathway and, 282–83
- nonselective cation channels and, 73–74

Hormonal response pathways

- nitrate signaling pathways and, 203

hot1 mutant

- temperature tolerance genes and, 229

HPL genes

- lipoxygenase pathway and, 285

HRT1 gene

- auxin signaling and, 380

hup1 gene

marine diatoms and, 122

hve mutant

- vascular tissue differentiation and pattern formation, 196

HYS gene

- phytochrome-dependent signaling and, 346

Hybrid holoenzymes

- Rubisco and, 459–60

Hydrostatic model of gravisensing

- root gravitropism and, 426–27

Hydroperoxy fatty acids

- lipoxygenase pathway and, 275–89

Hyperpolarization-activated NSCCs

- nonselective cation channels and, 73–77

Hypersensitive response

- plant responses to insect herbivory and, 300, 302

I

ids mutant

- rice as comparative genomics model and, 408

ifl1 mutant

- vascular tissue differentiation and pattern formation, 190–91, 196

Illegitimate integrative transformation

- complex evolution of photosynthesis and, 484

Imidazoles

- primary photochemistry of photosystem II and, 566
- immutans mutant
- chlororespiration and, 533, 538

Impatiens sultani

- cell separation processes and, 134

Indeterminant meristems

Arabidopsis meristem maintenance and, 49

Indirect defenses

- plant responses to insect herbivory and, 299, 301, 303–5, 316–19

Indole-3-acetic acid (IAA)

- cell separation processes and, 135, 143
- root gravitropism and, 432–33, 435–37

Induced acquired systemic resistance

- lipoxygenase pathway and, 287

Inflorescences

- grass
- rice as comparative genomics model and, 406–8

Insect herbivory

- plant responses to complexity and coordination of insect-induced responses, 320–21
- conclusions, 321
- costs of defense, 302–3
- crosstalk, 311–13
- differing plant responses to pathogens and herbivores, 300–2
- direct defenses, 303, 313–16
- elicitors from herbivores, 304–8
- extrafloral nectar, 319
- fitness-based evaluations of resistance traits, 302
- indirect defenses, 303–4, 316–19
- octadecanoids, 309–11
- terminology, 302–4
- tolerance, 304
- volatile organic compounds, 317–19
- wound signals, 308–9

wound-elecited responses, 308–13

I

Insertion vectors complex evolution of photosynthesis and, 485–86

Intermediary metabolism α -ketocid dehydrogenase complexes and, 357–70

Intracellular localization phytochrome-dependent signaling and, 334–39

In vivo spectroscopy phytochrome-dependent signaling and, 329–47

Ion channels nonselective cation channels and, 67–96

Ionic homeostasis signaling pathways salt and drought stress signal transduction, 247–67

Ionotropic glutamate receptors nonselective cation channels and, 91–93

Iron marine diatoms and, 109, 116–17, 119

isn1 mutant vascular tissue differentiation and pattern formation, 195

ixa mutant vascular tissue differentiation and pattern formation, 196

J

jar mutant cell separation processes and, 147

Jasmonates lipoxygenase pathway and, 275, 279–81, 286–89 plant responses to insect herbivory and, 305–6

jin mutant cell separation processes and, 147

JMT gene plant responses to insect herbivory and, 311

Jointless mutant cell separation processes and, 133

K

K^+ nonselective cation channels and, 68–70, 72, 76, 79–81, 83–84, 86–96 salt and drought stress signal transduction, 250–51

Kanamycin marine diatoms and, 122

KAT channel family nonselective cation channels and, 88, 90

KCO genes nonselective cation channels and, 93–94

α -Ketoacid dehydrogenase complexes branched-chain α -ketocid dehydrogenase, 365 regulation, 365 structure, 365–66 evolutionary considerations, 368–70 gene expression, 367 genomics, 366–67 introduction, 358–59 α -ketocid dehydrogenase complex, 366 mitochondrial pyruvate dehydrogenase complex, 359–63 plastidial pyruvate dehydrogenase complex, 363–65 prospectus, 370

α -Ketoglutarate regulation of lysine metabolism in plants and, 35

Kinase-associated protein phosphatase (KAPP) *Arabidopsis* meristem maintenance and, 53–54

Kinetics nonselective cation channels and, 81–84 phytochrome-dependent signaling and, 329, 331–34

primary photochemistry of photosystem II and, 551, 555, 557 Rubisco and, 451–54

KIN genes salt and drought stress signal transduction, 261–63, 265

KN1 transcription factor *Arabidopsis* meristem maintenance and, 62

L

La^{3+} nonselective cation channels and, 79

Lanthanides nonselective cation channels and, 85

LAP gene plant responses to insect herbivory and, 310

late dehiscence gene cell separation processes and, 146

Lateral roots nitrate signaling pathways and, 203, 209–12

lateral suppressor mutant cell separation processes and, 133

LATs nitrate signaling pathways

and, 205
lax-1 mutant
 rice as comparative genomics model and, 407
LCT1 gene
 nonselective cation channels and, 94–95
Leaf alcohols/aldehydes
 lipoxygenase pathway and, 275, 281–83, 285, 287–89
Leaf expansion
 nitrate signaling pathways and, 203, 214–16
Leaves
 cell separation processes and, 131–50
Lepidium spp.
 nonselective cation channels and, 85
 root gravitropism and, 429
LFY gene
Arabidopsis meristem maintenance and, 59–62
 rice as comparative genomics model and, 404–7
lhs1 mutant
 rice as comparative genomics model and, 408
LHY gene
 phytochrome-dependent signaling and, 341, 346
Ligand-receptor signal transduction pathway
Arabidopsis
 meristem maintenance and, 45, 52–54
Light
 marine diatoms and, 117–19
Light-dependent nuclear translocation/transcriptional complexes
 phytochrome-dependent signaling and, 329–47
Linum usitatissimum

lipoxygenase pathway and, 282–83
Lipid peroxidation
 lipoxygenase pathway and, 275–90
Lipids
 history of research, 14
 salt and drought stress signal transduction, 247, 255–58
 temperature tolerance genes and, 225, 227, 231–38
Lipoxygenase pathway
 conclusions, 289–90
 introduction, 276
LOX reaction, 276
 conclusions, 289–90
CYP74 gene, 283–86
 functional analysis, 286
 hydroxyperoxy fatty acid metabolism, 283–86
 intracellular localization, 279, 285–86
 oxylipin profiling, 286–88
 pathway, 280–89
 physiological functions, 279–80
 positional specificity, 277–79
 product specificity, 283–84
 regulation, 288–89
 substrate phylogenetic analysis, 278–79, 285
 substrate specificity, 278, 283–84
 transgenic plants, 286
LKR/SDH gene
 regulation of lysine metabolism in plants and, 37–39
Lolium spp.
 rice as comparative genomics model and, 406
Long-range signals

nitrate signaling pathways and, 207–9, 212–15
lop1 mutant
 vascular tissue differentiation and pattern formation, 196
los5 mutant
 salt and drought stress signal transduction, 265
Lotus spp.
 cell separation processes and, 145
 chlororespiration and, 528
LOX reaction
 lipoxygenase pathway and, 276–78
LpTFL1 gene
 rice as comparative genomics model and, 407
L77 genes
 salt and drought stress signal transduction, 261–63, 265
Lycopersicon esculentum
 cell separation processes and, 135
 α -ketoacid dehydrogenase complexes and, 368–69
 lipoxygenase pathway and, 282–83
 nonselective cation channels and, 77
Lycopersicon peruvianum
 plant responses to insect herbivory and, 309, 311
Lysine
 regulation of metabolism in plants and
 α -amino adipic acid pathway, 36–37
 catabolism, 34–39
 conclusions, 39–40
 developmental signals, 32–33
 environmental signals, 32–33
 feedback inhibition

loops, 28–31
 future research, 39–40
 introduction, 28
LKR/SDH in plants and animals, 39
 metabolic interactions between aspartate-family amino acids and amide amino acid metabolism, 33–34
 physiological signals, 32–33
 random distribution of aspartate-family pathway enzymes and metabolites in plastids, 31–32
 seed development, 34–36

Lysine-ketoglutarate reductase
 regulation of lysine metabolism in plants and, 35–39

M

Macaranga tanarius
 plant responses to insect herbivory and, 319

MADS-box genes
 cell separation processes and, 133
 rice as comparative genomics model and, 408–9

Magnaporthe grisea
 rice as comparative genomics model and, 409

Manuda sexta
 plant responses to insect herbivory and, 305–7, 309, 312–13, 320–21

Mantionella squamata
 chlororespiration and, 536

Marchantia polymorpha
 chlororespiration and, 528
 complex evolution of

photosynthesis and, 510
***MAR* genes**
 root gravitropism and, 430

Marine diatoms
 biology
 cell division, 112–13
 cell wall biogenesis, 112–13
 general characteristics, 111–12
 light, 117–19
 neighbor perception, 117
 nutrients, 116–17
 photosynthesis, 114–16
 sex, 113–14
 ecosystem Earth, 109–11
 model species, 121–25
 phylogeny, 120–21
"Master switch"
 lipoxygenase pathway and, 289

Mastogloia binotata
 marine diatoms and, 111

Mayaudon J. 13–14

***mbl* mutant**
 vascular tissue
 differentiation and pattern formation, 196

Mechanosensing
 root gravitropism and, 421–40

Mechanosensitive NSCCs
 nonselective cation channels and, 75, 79–80

Medicago spp.
 lipoxygenase pathway and, 282–85

Membrane lipids
 history of research, 14–22
 temperature tolerance genes and, 225, 227, 231–38

Meristem
Arabidopsis meristem maintenance and, 45–62

Meristem identity genes
 rice as comparative

genomics model and, 402

Mesostigma viride
 α -ketoadic dehydrogenase complexes and, 368–69

Metabolic engineering
 α -ketoadic dehydrogenase complexes and, 357

Metabolic flux
 regulation of lysine metabolism in plants and, 27

Metabolic profiling
 lipoxygenase pathway and, 275, 283–88, 290

Metabolism
 α -ketoadic dehydrogenase complexes and, 357–70
 lysine and, 27–40

Metallothioneins
 heavy metal detoxification and homeostasis, 159–78

Methanobacterium thermoautotrophicum
 complex evolution of photosynthesis and, 510

Methanococcus janaschii
 complex evolution of photosynthesis and, 510

Methanol
 history of research, 1

Metric system
 history of research, 21–22

Mg²⁺
 α -ketoadic dehydrogenase complexes and, 362
 nonselective cation channels and, 69–70, 76, 80–85, 89, 96
 Rubisco and, 451–52

Mg-tetrapyrrole biosynthesis
 complex evolution of photosynthesis and, 503–25

Microarray technology
 rice as comparative
 genomics model and, 402

midribless mutant
vascular tissue
differentiation and pattern formation, 196

Mitochondria
chlororespiration and, 523, 537
 α -ketoacid dehydrogenase complexes and, 357

Mitochondrial pyruvate dehydrogenase
 α -ketoacid dehydrogenase complexes and, 357, 359–63

Mitogen-activated protein kinases (MAPKs)
Arabidopsis meristem maintenance and, 53–54
salt and drought stress signal transduction, 247, 253–55

Molecular breeding
temperature tolerance genes and, 225–26

Moss
targeted mutagenesis in *Physcomitrella patens* and, 477–95

MP genes
vascular tissue
differentiation and pattern formation, 189–91, 196

ms35 (msh) mutant
cell separation processes and, 146

MSG1 gene
root gravitropism and, 437

MT genes
phytochelatins and metallothioneins, 173–78

Musa acuminata
lipoxygenase pathway and, 282–83

Mutualism
plant responses to insect herbivory and, 303

Myzus persicae

plant responses to insect herbivory and, 310, 312

N

NII gene
nitrate signaling pathways and, 207

Na⁺
nonselective cation channels and, 68, 71, 76–80, 84, 87–88, 90–91, 94–96
salt and drought stress signal transduction, 247–67

NADP⁺
chlororespiration and, 423–42

Nanotechnology industry
marine diatoms and, 109, 122

NaPMT genes
plant responses to insect herbivory and, 313

Narcissus pseudonarcissus
chlororespiration and, 538

Nar genes
nitrate signaling pathways and, 206

NAT genes
marine diatoms and, 116–17

Ndh gene complex
chlororespiration and, 528–30, 532–41

NEEDLY gene
rice as comparative genomics model and, 406

Neighbor perception
marine diatoms and, 117

Neisseria meningitidis
 α -ketoacid dehydrogenase complexes and, 368–69

Nephroselmis olivacea
chlororespiration and, 528
complex evolution of photosynthesis and, 514

Neurospora crassa
nitrate signaling pathways and, 206

Neutron activation chromatography
history of research, 1, 16–17

NFL genes
rice as comparative genomics model and, 406

NIA gene
nitrate signaling pathways and, 205–7

Nicotiana alata
plant responses to insect herbivory and, 315

Nicotiana attenuata
plant responses to insect herbivory and, 306–7, 321

Nicotiana plumbaginifolia
nitrate signaling pathways and, 205
phytochrome-dependent signaling and, 336

Nicotiana sylvestris
plant responses to insect herbivory and, 311

Nicotiana tabacum
chlororespiration and, 528
plant responses to insect herbivory and, 311, 313

Nifedipine
nonselective cation channels and, 69

NifH gene
complex evolution of photosynthesis and, 510

Nitella flexilis
nonselective cation channels and, 74, 77

Nitrate signaling pathways
AiNRT1.1 nitrate transporter, 211–12
auxins, 212–14
conclusions, 215–17
diurnal regulation, 209–10
feedback regulation by N

status of plant, 207–8
 induction of nitrate transporter genes, 205
 introduction, 203–4
 lateral roots
 development, 212
 elongation, 209–11
 growth, 209–12
 outgrowth, 211–12
 leaf expansion, 214–16
 local signals, 209–12
 long-range signals, 207–9, 212–15
 N status of shoot
 communicated to root, 208–9
 regulation of growth and development, 209–15
 regulation of nitrate uptake, 205–9
 root branching, 212–14
 shoot control of lateral root development, 212
 signal transduction pathway for nitrate induction of gene expression, 206–7
 sugar signaling, 209–10, 214
Nonselective cation channels (NSCCs)
 AKT family, 90
AtCCH1, 91
 Ca^{2+} -activated NSCCs, 78
 cation transporters of nonchannel topology, 94–95
 cautionary note, 86–87
 conclusions, 96
 cyclic nucleotide-gated NSCCs, 78–79, 87–90
 definition, 68–69
 depolarization-activated NSCCs, 72
 early observations, 71, 72
 endoplasmic reticulum, 85
 experimental characterization, 70–71
 fast-activating NSCCs, 83–84
 gating and kinetics, 81–84
 glutamate-activated NSCCs, 79
 GORK family, 90
 hyperpolarization-activated NSCCs, 73–77
 introduction, 68
 ionotropic glutamate receptors, 91–93
 KAT family, 90
 mechanosensitive NSCCs, 75, 79–80
 miscellaneous channel sequences, 93–94
 miscellaneous endomembranes, 84–85
 molecular characterization, 85–93
 plasma membrane, 72–80
 reasons for existence of NSCCs, 95–96
 selectivity, 80–81, 83
SKOR family, 90
 slow-activating NSCCs, 80–83
 symbiosome membranes, 85
 tonoplast, 80–84
 unitary conductance, 81, 83
 voltage-gated ion channel superfamily, 87–91
 voltage-insensitive NSCCs, 77–78
Nourseothricin marine diatoms and, 122
NPDK2 gene phytochrome-dependent signaling and, 342–43
NPH4 gene root gravitropism and, 437
NpNRT2.1 gene nitrate signaling pathways and, 208
npr1 mutant plant responses to insect herbivory and, 312
NPR1/NIM1 gene rice as comparative genomics model and, 412–13
NRT genes nitrate signaling pathways and, 205–12
NtFAD3 gene temperature tolerance genes and, 235
Nuclear speckles phytochrome-dependent signaling and, 336–38
Nucleo/cytoplasmic partitioning phytochrome-dependent signaling and, 335–39
Nucleus phytochrome-dependent signaling and, 329–47

O
Ocean marine diatoms and, 109–25
Ocean lipids history of research, 14–22
Octadecanoids plant responses to insect herbivory and, 305, 309–11
ohr1 mutant phytochrome-dependent signaling and, 340
Old Radiation Laboratory (ORL), 1, 9–10, 13, 22
12-OPDA reductase gene plant responses to insect herbivory and, 310
Organ shedding cell separation processes and, 131–35
Orthologous genes rice as comparative

genomics model and, 399–413

Oryza sativa

- chlororespiration and, 528–29
- comparative genomics model and, 399–413

Oshox1 gene

- vascular tissue differentiation and pattern formation, 189

OsMADS genes

- rice as comparative genomics model and, 408–9

Osmotic homeostasis

- signaling pathways
- salt and drought stress
- signal transduction, 247–67

Osmotic stress

- salt and drought stress
- signal transduction, 247–67

Oxidases

- chlororespiration and, 523, 533–34

Oxidation

- Rubisco and, 449–65

2-Oxoglutarate dehydrogenase

- α -ketoadic dehydrogenase complexes and, 357

Oxygen

- complex evolution of photosynthesis and, 503–25
- plant responses to insect herbivory and, 308
- primary photochemistry of photosystem II and, 551–71

Rubisco and, 449–65

temperature tolerance genes and, 225, 227, 229–30

Oxylipin

lipoxygenase pathway and, 275

P

P^+ cation localization

primary photochemistry of photosystem II and, 558–61

P680

- primary photochemistry of photosystem II and, 551

Papaver somniferum

- cell separation processes and, 149

Paper chromatography

- history of research, 11–12, 17

Paracoccus denitrificans

- complex evolution of photosynthesis and, 514

Parthenium argentatum

- lipoxygenase pathway and, 282–83

Pasteurella multocida

- α -ketoadic dehydrogenase complexes and, 368–69

PAT1 gene

- phytochrome-dependent signaling and, 342

Pathogenesis-related proteins

- cell separation processes and, 139

Pathogens

- lipoxygenase pathway and, 275
- plant responses to insect herbivory and, 299–302, 305–6
- rice as comparative genomics model and, 409

Pathway crosstalk

- plant responses to insect herbivory and, 301, 311–13

Pattern formation

- Arabidopsis* meristem maintenance and, 45–62

marine diatoms and, 109

vascular tissue differentiation and, 183–97

Pattern recognition

- history of research, 12

Pb^{2+}

- nonselective cation channels and, 89

Pcs1 gene

- phytochelatins and metallothioneins, 162

PC synthases

- phytochelatins and metallothioneins, 159, 161–65, 167

PDF1.2 gene

- plant responses to insect herbivory and, 312

Petroselinum crispum

- nonselective cation channels and, 74

PGAZAT gene

- cell separation processes and, 137–38

pgm mutants

- root gravitropism and, 439

Phaeodactylum tricornutum

- chlororespiration and, 536
- marine diatoms and, 114–15, 117, 121–24

phan mutant

- vascular tissue differentiation and pattern formation, 194

Phaseolus vulgaris

- cell separation processes and, 134–36, 139
- nonselective cation channels and, 73–74

phb-1d mutant

- vascular tissue differentiation and pattern formation, 194

Phenolic proton

- tyrosine primary photochemistry

of photosystem II and, 567–68

Pheophytins
primary photochemistry of photosystem II and, 551, 553–55, 557, 560–61, 563–64, 566, 570

Phleomycin
marine diatoms and, 122

Phloem
vascular tissue
differentiation and pattern formation, 183–97

Phosgene
history of research, 8–9

Phosphate
regulation of lysine metabolism in plants and, 33

Phosphatidylglycerol
history of research, 15–16
temperature tolerance genes and, 232–33

Phospholipids
lipoxygenase pathway and, 278, 285
salt and drought stress signal transduction, 247, 255–58

Phosphorus
membrane lipids and history of research, 1, 6

Photochemistry
primary
photosynthesis and, 551–71

Photomorphogenesis
phytochrome-dependent signaling and, 329–47

Photopigments
complex evolution of photosynthesis and, 503–25

Photoreceptor interacting network
phytochrome-dependent signaling and, 332–34

Photospiration
Rubisco and, 449–65

Photosynthesis
chlororespiration and, 523, 537
complex evolution of carotenoid biosynthesis genes, 517–18
conclusions, 518
Cre/lox-mediated site-specific recombination, 492–94
cytochrome *bc* complex, 517
episomal replicative transformation, 482–84
functional studies of promoters, 489–90
gene function analysis, 487–89
geochemical evidence, 505–7
heterologous conditional promoters, 490–92
illegitimate integrative transformation, 484
insertion vectors, 485–86
introduction, 504
Mg-tetrapyrrole biosynthesis, 507–10
nonphotosynthesis-related molecular markers, 507
oxygenic photosynthesis, 516–17
reaction center apoproteins, 511–15
replacement vectors, 486–87
targeted mutagenesis concepts, 484–85
theories of origin, 505–7
transformation, 485–87
unified model for origin and evolution of reaction centers, 515–16
history of research, 1–23
marine diatoms and, 109–25
nitrate signaling pathways and, 210, 213
regulation of lysine metabolism in plants and, 33–34
Rubisco and, 449–65

Photosystem I (PSI)
chlororespiration and, 523, 539–40

Photosystem II (PSII)
primary photochemistry of alternate electron donors, 568–70
 B_A , 559–60
bacterial reaction centers, 557–58
 B_B , 560
 Chl_{ZD1} , 560–61
 Chl_{ZD2} , 560–61
conclusions, 571
donor-side secondary electron transfer, 566–67
electrostatics, 567–68
energy transfer, 555–57
introduction, 552
 3P reaction center triplet, 561
 P^+ cation localization, 558–61
 P_A , 558–59
 P_B , 559
 $Pheo_A$, 560
 $Pheo_{AB}$, 560
primary charge separation, 562–66
reevaluation of energetics, 570–71
sharing of cation radical, 562
spectra of PSII reaction center chlorins, 558–61

structure, 552–55
tyrosine phenolic proton, 567–68

temperature tolerance
genes and, 233

Phototransduction
phytochrome-dependent
signaling and, 340–43

Phycobilisomes
marine diatoms and, 117, 120

Phyllotreta spp.
plant responses to insect
herbivory and, 315–16

Phylogenetic analysis
complex evolution of
photosynthesis and, 503–25

lipoxygenase pathway and, 278–79, 285

marine diatoms and, 120–21

rice as comparative
genomics model and, 406

Physcomitrella patens
lipoxygenase pathway and, 282–85

targeted disruption, 487–89

targeted mutagenesis in
conclusions, 494–95

genetic transformation, 481–94

introduction, 477–80

methodological
development, 489–94

model system, 480–81

transformation with
DNA carrying
homologous sequences, 484–87

transformation with
DNA without
homology, 481–84

Phytochelatins
heavy metal detoxification
and homeostasis, 159–78

Phytochelatins/metallothioneins

introduction, 160–61

metallothioneins
function, 177

future research, 177–78

gene expression, 174–76

gene structure, 172–73

proteins, 173–74

structure, 170–76

PC synthase enzymes, 167

phytochelatins
animal PC synthase
expression, 163–65

biosynthetic pathway, 161

metals other than Cd, 168–69

PC synthase enzymes, 165

PC synthase genes, 161–65

roles, 169–70

sequestration to vacuole, 167–68

structure, 161

sulfide ions, 168

**Phytochrome-dependent
signaling**
photomorphogenesis
controlled by
conclusions, 346–47

genetic approaches, 339–43, 346–47

genetic phytochrome
signaling, 343–46

inactivation of
phyB-mediated
signaling, 337

intracellular localization, 334–39

introduction, 330–31

kinetics, 331–34

molecular approaches, 339–43

nuclear speckles, 336–37

nucleo/cytoplasmic
partitioning and
phyA/phyB/phyC-E

import into nucleus, 335–39

photoreceptor
interacting network, 332–34

phyA phototransduction
pathway, 342–43

phyB phototransduction
pathway, 340–42

phyB transport in
nucleus, 337

spectroscopy, 331–32

Phytophthora spp.
lipoxygenase pathway and, 280, 286

nonselective cation
channels and, 77

Phytoremediation
phytochelatins and
metallothioneins, 178

Picea spp.
 α -ketoacid dehydrogenase
complexes and, 362

phytochelatins and
metallothioneins, 171

Pieris brassicae
plant responses to insect
herbivory and, 304, 320

PIF3 gene
phytochrome-dependent
signaling and, 341–43, 346

Pi genes
plant responses to insect
herbivory and, 312

rice as comparative
genomics model and, 410

PIN1 gene
root gravitropism and, 433–35

vascular tissue
differentiation and pattern
formation, 189, 196

Pin2 gene
plant responses to insect
herbivory and, 308, 310–11

PINOID gene
 vascular tissue
 differentiation and pattern formation, 190

Pinus spp.
 chlororespiration and, 534
 rice as comparative genomics model and, 406

Pinus thunbergii
 chlororespiration and, 528
 complex evolution of photosynthesis and, 510, 514

PIP5K gene
 salt and drought stress signal transduction, 256

Pisum sativum
 α -ketoadic dehydrogenase complexes and, 368–69

PKS1 gene
 phytochrome-dependent signaling and, 342–44

Plant sulfolipid
 history of research, 14, 16

Plantago spp.
 nonselective cation channels and, 80, 82

Plasma membrane
 nonselective cation channels and, 67, 72–80

Plastidial pyruvate dehydrogenase
 α -ketoadic dehydrogenase complexes and, 357

Plastidial pyruvate dehydrogenase complex
 α -ketoadic dehydrogenase complexes and, 363–65

Plastids
 chlororespiration and, 423–42
 marine diatoms and, 114, 120
 regulation of lysine metabolism in plants and, 31, 33

Plastid-terminal oxidase

chlororespiration and, 523, 533

Plastoquinones
 chlororespiration and, 423–42

Plectonema boryanum
 complex evolution of photosynthesis and, 510

Pleurochloris meiringensis
 chlororespiration and, 533, 536

Pleurosira laevis
 marine diatoms and, 118

Pluripotent stem cells
Arabidopsis meristem maintenance and, 45–62

Pod dehiscence
 cell separation processes and, 131, 140–43

POL gene
Arabidopsis meristem maintenance and, 57–59, 61–62

Pollution
 phytochelatins and metallothioneins, 178

Polygalacturonase
 cell separation processes and, 137–38, 143–44

Polyunsaturated fatty acids (PUFAs)
 lipoxygenase pathway and, 275–89
 temperature tolerance genes and, 234, 237–38

Porphyra purpurea
 chlororespiration and, 528
 complex evolution of photosynthesis and, 510
 α -ketoadic dehydrogenase complexes and, 368–69

Porphyrins
 marine diatoms and, 119

Posidonia oceanica
 nonselective cation channels and, 80

phytochelatins and metallothioneins, 176

Positional cloning
 rice as comparative genomics model and, 402

Positional specificity
 lipoxygenase pathway and, 277–79

Posttranscriptional regulation
 chlororespiration and, 538–39
 regulation of lysine metabolism in plants and, 27

PRFL gene
 rice as comparative genomics model and, 406

PR genes
 plant responses to insect herbivory and, 312–13

Primary charge separation
 primary photochemistry of photosystem II and, 551, 555–58, 562–66, 570

Procambium
 vascular tissue
 differentiation and pattern formation, 188–90

Product specificity
 lipoxygenase pathway and, 283–84

Proline
 regulation of lysine metabolism in plants and, 38

Promoters
 complex evolution of photosynthesis and, 489–90

prosystemin gene
 plant responses to insect herbivory and, 310

Proteasome
 auxin signaling and, 381

Protein kinases
 α -ketoadic dehydrogenase complexes and, 357

salt and drought stress

signal transduction, 247, 253–55

P

Protein phosphatases
α-ketoacid dehydrogenase complexes and, 357

Pseudomonas aeruginosa
α-ketoacid dehydrogenase complexes and, 368–69

Pseudomonas syringae
plant responses to insect herbivory and, 312

Psidium guajava
lipoxygenase pathway and, 282–83

Purple nonsulfur
photosynthetic bacteria
primary photochemistry of photosystem II and, 551–71

Putrescine
plant responses to insect herbivory and, 305–6

Pyruvate dehydrogenase
α-ketoacid dehydrogenase complexes and, 357, 359–64

Q

Quantitative trait loci (QTLs)
cell separation processes and, 145

Quorum sensing
marine diatoms and, 109, 119

R

Rac small G protein genes
rice as comparative
genomics model and, 411

Radiochromatographic exploration
history of research, 1, 14–22

RAP genes
rice as comparative

Rapeseed
regulation of lysine metabolism in plants and, 36

Rat House, 1, 5–8

Rb^+
nonselective cation channels and, 83

rbc mutants
Rubisco and, 451, 455–56

RBX1 gene
auxin signaling and, 380, 382

rca mutant
Rubisco and, 462

RD genes
salt and drought stress signal transduction, 261–65

RDPG1 gene
cell separation processes and, 143–44

Reaction center
complex evolution of photosynthesis and, 503–25

primary photochemistry of photosystem II and, 551, 553–61, 564–65

Reactive oxygen species
cell separation processes and, 139

nonselective cation channels and, 67

plant responses to insect herbivory and, 308

Red algae
chlororespiration and, 528

marine diatoms and, 120

Rubisco and, 454

RED1 gene
phytochrome-dependent signaling and, 340–41

genomics model and, 405, 408–9

Redox
chlororespiration and, 423–42

Replacement vectors
complex evolution of photosynthesis and, 486–87

Reproductive development
rice as comparative
genomics model and, 399, 402–9

Respiration
chlororespiration and, 423–42

Rubisco and, 449–65

Restriction fragment length polymorphisms (RFLPs)
cell separation processes and, 145

Reverse electron flow
chlororespiration and, 532–33

Reverse genetic profiling
lipoxygenase pathway and, 275

Reversible radical pair model
primary photochemistry of photosystem II and, 555

RFL gene
rice as comparative
genomics model and, 405

R-genes
plant responses to insect herbivory and, 300

rice as comparative
genomics model and, 410

RHG gene
root gravitropism and, 429–30

Rhizobium phaseolis
complex evolution of photosynthesis and, 510

Rho-like GTPases
Arabidopsis meristem maintenance and, 53–54

Rhodobacter capsulatus
complex evolution of

photosynthesis and, 510, 514

Rhodobacter sphaeroides
chlororespiration and, 539
complex evolution of photosynthesis and, 510, 514

primary photochemistry of photosystem II and, 553–57, 559, 564

Rhodobacter viridis
primary photochemistry of photosystem II and, 553

Rhodopsin
marine diatoms and, 117–18

Rhodospirillum rubrum
complex evolution of photosynthesis and, 510
history of research, 14

Rubisco and, 451, 454–55, 459

Rice
comparative genomics model and
conclusions, 413
defense signaling, 409–13
disease resistance, 409–10
EST database, 401
floral organ development genes, 408–9
gene-tagged lines, 401
genome sequencing, 400–1
heterotrimeric G protein, 411–12
introduction, 400
meristem determinacy in grass inflorescences, 406–8
meristem identity genes in grasses, 404–6
microarray technology, 402

NPR1/NIM1 gene, 412–13

positional cloning, 402

Rac small G-protein genes, 411

reproductive development, 402–9

Ricinus communis
nitrate signaling pathways and, 208

Rickettsia prowazekii
 α -ketoacid dehydrogenase complexes and, 368–69

Ripening
cell separation processes and, 131, 137

ROCI gene
auxin signaling and, 380

Root gravitropism
ARG/RHG, 429–30
AGRI-like proteins, 434–35

ARL2, 429–30

auxin-gradient-independent phase, 437–39

auxin-response mutants, 435

auxins, 430–37
conclusions, 439–40
cytosolic pH, 428–29
efflux carrier complexes, 432–34

gravireceptor(s), 427–28
gravisensing, 424–26
hydrostatic model of gravisensing, 426–27

introduction, 422
lateral auxin gradient across root caps, 434–35

morphogenesis, 423

protein degradation pathway, 435

root-curvature response, 435–37

second messengers, 428–29

signal transduction/signal transmission, 428–32

starch-statolith hypothesis of gravity sensing, 424–26

tip-curvature response, 424

transcriptional regulation, 435–37

Roots
cell separation processes and, 148–49
cell separation processes and, 131–50
nitrate signaling pathways and, 203, 208–9

Rotenone
chlororespiration and, 538

RPM1 gene
rice as comparative genomics model and, 410

RPP5 gene
rice as comparative genomics model and, 410

RPS2 gene
rice as comparative genomics model and, 410

RUBI gene
auxin signaling and, 385–88

Rub S, 1, 5–9

Rubia tinctorum
phytochelatins and metallothioneins, 169

Rubisco
activase, 461–65
barrel structures, 458–59
catalysis, 451–52
 CO_2/O_2 specificity, 452–53
conformational changes, 452
defining a better enzyme, 453–54
first partial reaction, 451–52
hybrid holoenzymes, 459–60
introduction, 450

kinetics, 451–54
 large subunit interactions, 455–59
 loop-6 amino-acid substitutions, 456–58
 marine diatoms and, 114
 mutational approaches, 455–56
 prospects for improvement, 465
 second partial reaction, 452–53
 selection for a better enzyme, 454–55
 sequences, 450–51
 small-subunit β A- β B loop, 460–61
 small subunit interactions, 459–61
 structure/function relationships, 450–55

Rubrivivax gelatinosus
 complex evolution of photosynthesis and, 510

S

SAC genes
 cell separation processes and, 143–45

Saccharomyces cerevisiae
 auxin signaling and, 380
 α -ketoacid dehydrogenase complexes and, 368–69
 marine diatoms and, 124
 nonselective cation channels and, 86, 91, 94–95
 phytochelatins and metallothioneins, 161–63, 167
 salt and drought stress signal transduction, 260

Saccharopine dehydrogenase
 regulation of lysine metabolism in plants and, 35–39

Salmon lipids

history of research, 14–22

Salt and drought stress
 signal transduction and
 abscisic acid, 258–66
 biosynthesis, 259
 degradation, 259
 future research, 266–67
 gene expression, 259–63
 inputs, 248–50
 introduction, 248
 osmotic stress signaling, 253–66
 outputs, 248–50
 protein kinase pathways, 253–55
SOS regulatory pathway for ion homeostasis and salt tolerance, 250–53
 water stress tolerance, 258–59

Sambucus nigra
 cell separation processes and, 135–36, 139

Scenedesmus spp.
 chlororespiration and, 527
 history of research, 14, 21

SCF^{TIR1} gene
 auxin signaling and, 377, 382–88

Schizosaccharomyces pombe
 phytochelatins and metallothioneins, 161–65, 167–69, 177–78

SE5 gene
 rice as comparative genomics model and, 403

SEC62 genes
 nonselective cation channels and, 94

Secale cereale
 nonselective cation channels and, 72–75

Second messengers
 phytochrome-dependent signaling and, 335
 root gravitropism and, 421–40

salt and drought stress
 signal transduction, 247

Secondary wall thickening
 vascular tissue
 differentiation and pattern formation, 192–93

Seeds
 cell separation processes and, 131–50
 regulation of lysine metabolism in plants and, 34–36

Sequestered areas of phytochrome (SAPs)
 phytochrome-dependent signaling and, 334

Sequestration to vacuole
 phytochelatins and metallothioneins, 167–68

Sex
 marine diatoms and, 113–14

sfc mutant
 vascular tissue
 differentiation and pattern formation, 196

Shibata K, 10–11

Shoot apical meristem
Arabidopsis meristem maintenance and, 45–62

Shoots
 nitrate signaling pathways and, 208–9, 212

SHP genes
 cell separation processes and, 133, 141, 147

Sig genes
 marine diatoms and, 114

Signal transduction
Arabidopsis meristem maintenance and, 45, 52, 55–56
 auxin signaling and, 377–92
 marine diatoms and, 117, 119
 nitrate signaling pathways

and, 203–17
phytochrome-dependent
 signaling and, 329–47
plant responses to insect
 herbivory and, 301,
 308–9
rice as comparative
 genomics model and, 399,
 409–13
root gravitropism and,
 421–40
salt and drought stress
 signal transduction,
 247–67
Sig natosome
 phytochrome-dependent
 signaling and, 334
Silene spp.
 phytochelatins and
 metallothioneins, 165–66,
 171, 177
Silica
 marine diatoms and,
 109–25
Sinapis alba
 cell separation processes
 and, 145
Siroheme
 phytochelatins and
 metallothioneins, 168
SIT genes
 marine diatoms and, 113
Skeletonema costatum
 marine diatoms and, 123
SKOR channel family
 nonselective cation
 channels and, 87, 90
Slow-activating NSCCs
 nonselective cation
 channels and, 80–83
SLR1 gene
 phytochrome-dependent
 signaling and, 340
SLW3 gene
 plant responses to insect
 herbivory and, 312
Sodium azide

chlororespiration and,
 538
Solanum tuberosum
 lipoxygenase pathway and,
 282–83
Soret absorption maximum
 primary photochemistry of
 photosystem II and, 559,
 567
Sorghum spp.
 phytochrome-dependent
 signaling and, 333
 plant responses to insect
 herbivory and, 315
SgOS regulatory pathway
 salt and drought stress
 signal transduction, 247,
 250–53, 257
SPA1 gene
 phytochrome-dependent
 signaling and, 342,
 345–46
Spatial feedback loop
Arabidopsis meristem
 maintenance and, 45,
 56–59
Spatial patterns
 plant responses to insect
 herbivory and, 299
Spectroscopy
 phytochrome-dependent
 signaling and, 331–32
 primary photochemistry of
 photosystem II and,
 558–61
Spinacia oleracea
 chlororespiration and, 528
 complex evolution of
 photosynthesis and, 514
Spodoptera spp.
 plant responses to insect
 herbivory and, 304–5, 314
SPT gene
 cell separation processes
 and, 141
Sr²⁺
 nonselective cation

channels and, 76
Ssy1 gene
 auxin signaling and, 380
Starch-statolith hypothesis of
 gravity sensing
 root gravitropism and,
 424–26
Stem cells
Arabidopsis meristem
 maintenance and, 45–62
 targeted mutagenesis in
Physcomitrella patens
 and, 477
Stems
 cell separation processes
 and, 131–50
STM gene
Arabidopsis meristem
 maintenance and, 56
Stress
 chlororespiration and,
 540–41
 lipoxygenase pathway and,
 275–76, 290
 plant responses to insect
 herbivory and, 301
 regulation of lysine
 metabolism in plants and,
 37–39
 temperature tolerance
 genes and, 225–39
Sub-freezing temperatures
 temperature tolerance
 genes and, 225–26
Submicrometer-scale silica
 structures
 marine diatoms and, 109,
 122
Substrate channeling
 α -ketoacid dehydrogenase
 complexes and, 357
Substrate specificity
 lipoxygenase pathway and,
 278, 283–84
Sucrose
 cell separation processes
 and, 145, 147

regulation of lysine metabolism in plants and, 33–34

Sugar signaling
nitrate signaling pathways and, 203, 209–10, 214, 217

Suicide trigger
marine diatoms and, 119

Sulfide ions
phytochelatins and metallothioneins, 168

Sulfolipids
history of research, 14, 16

Sulfur
membrane lipids and, 1

Surfactants
history of research, 14, 16

Symbiosome membranes
nonselective cation channels and, 85

Synechococcus sp.
complex evolution of photosynthesis and, 510, 514
phytochelatins and metallothioneins, 170, 174
primary photochemistry of photosystem II and, 552, 554
Rubisco and, 451, 455–61

Synechocystis sp.
chlororespiration and, 530, 539
complex evolution of photosynthesis and, 510, 514
 α -ketoacid dehydrogenase complexes and, 368–69
nonselective cation channels and, 92
primary photochemistry of photosystem II and, 562, 566, 568–69

Systemic wound signals
plant responses to insect herbivory and, 305

T

TaFAD3 gene
temperature tolerance genes and, 238

Tamiya H, 10–11, 15

TaPCS1 gene
phytochelatins and metallothioneins, 161, 167

TAPG genes
cell separation processes and, 137

Targeted degradation
auxin signaling and, 377, 380–82

Targeted mutagenesis
complex evolution of photosynthesis and, 484–85
targeted mutagenesis in *Physcomitrella patens* and, 477–95

TEA⁺
nonselective cation channels and, 68–70, 81

TED3 gene
vascular tissue differentiation and pattern formation, 188

Temporal patterns
plant responses to insect herbivory and, 299

Temporal signaling systems
Arabidopsis meristem maintenance and, 45–62

TFL1 gene
rice as comparative genomics model and, 404, 407–8

Thalassiosira spp.
marine diatoms and, 114, 124–25

Threonine
regulation of lysine metabolism in plants and, 29–31, 34

Thylakoid membranes
chlororespiration and, 423–42

TIR1 gene
auxin signaling and, 377, 382–88

TMA⁺
nonselective cation channels and, 81

TOC1 gene
phytochrome-dependent signaling and, 346

Tolerance
plant responses to insect herbivory and, 299, 304

Tonoplasts
nonselective cation channels and, 67, 80–84

Top-down processes
plant responses to insect herbivory and, 313

Topology
nonselective cation channels and, 94–95

Tracheary element formation
vascular tissue differentiation and pattern formation, 183–97

trans-activating elements
plant responses to insect herbivory and, 299, 321

Transcriptional activation
salt and drought stress signal transduction, 247, 261–67

Transcriptional reconfiguration
plant responses to insect herbivory and, 305–6

Transcriptional regulation
auxin signaling and, 377–92
chlororespiration and, 538–39
regulation of lysine

metabolism in plants and, 27
 root gravitropism and, 435–37

Transcriptome
 plant responses to insect herbivory and, 320

Transformation
 complex evolution of photosynthesis and, 485–87

Transgenes
Arabidopsis meristem maintenance and, 55 auxin signaling and, 385 cell separation processes and, 136–37, 144 lipoxygenase pathway and, 280, 286 marine diatoms and, 116, 122 nitrate signaling pathways and, 215 phytochrome-dependent signaling and, 337 plant responses to insect herbivory and, 311 regulation of lysine metabolism in plants and, 32, 35–37, 39 temperature tolerance genes and, 232–33, 235–38

Trans-splicing
 regulation of lysine metabolism in plants and, 38

Transposons
 vascular tissue differentiation and pattern formation, 191

Trap limited model
 primary photochemistry of photosystem II and, 555–56

Trichoderma viridae
 plant responses to insect herbivory and, 306

Trichoplysia ni
 plant responses to insect herbivory and, 316

Tridacna maxima
 history of research, 20

Trienoic fatty acids
 temperature tolerance genes and, 235–37

Tris⁺
 nonselective cation channels and, 68, 81

Triticum aestivum
 nonselective cation channels and, 73–75

Tryptophan
 auxin signaling and, 377–92

Two-hybrid screen
 yeast regulation of lysine metabolism in plants and, 30

Tyrosine
 primary photochemistry of photosystem II and, 567–68

U

Unicellular photosynthetic eukaryotes
 marine diatoms and, 109–25

UNI gene
 rice as comparative genomics model and, 406

Unitary conductance
 nonselective cation channels and, 81, 83

V

Vacuoles
 phytocelatins and metallothioneins, 167–68

van mutants
 vascular tissue differentiation and pattern formation, 196

Vascular tissue differentiation pattern formation and approaches for studying vascular development, 187–88

Arabidopsis, 187 cambium, 188–90 cell death, 193 cell elongation, 192 *Coleus*, 186 conclusions, 197 introduction, 184 model systems, 186–87 pattern formation, 193–96 procambium, 188–90 process of vascular differentiation, 188–93 secondary wall thickening, 192–93 vascular bundles, 193–95 vascular patterning at organ level, 195–96 vascular patterns, 185–86 vascular tissue organization at organ level, 185–86 visualization of vascular tissues, 188 xylem differentiation, 190–91 *Zinnia*, 186

“Venus fly-trap” mechanism nonselective cation channels and, 92

Verapamil
 nonselective cation channels and, 69, 85

Vibronic fine structure
 primary photochemistry of photosystem II and, 562, 569

Vicia faba
 nonselective cation

channels and, 74, 76, 82–83
phytochelatins and metallothioneins, 175
salt and drought stress signal transduction, 256

Vigna unguiculata
nonselective cation channels and, 81

Volatile organic compounds (VOCs)
plant responses to insect herbivory and, 303–7, 313, 317–19

Volatiles
lipoxygenase pathway and, 275, 281–83, 285, 287–89

Voltage gating
nonselective cation channels and, 67, 77–79, 81, 82, 83, 84, 87–91
salt and drought stress signal transduction, 253

***vsp1* mutant**
lipoxygenase pathway and, 279

W

Water
chlororespiration and, 423–42

Water stress signaling
salt and drought stress signal transduction, 247–67

Wax ester
history of research, 18–19

wilted mutant
vascular tissue differentiation and pattern formation, 191

wilty-dwarf mutant
vascular tissue differentiation and pattern formation, 191

***WOL* gene**
vascular tissue

differentiation and pattern formation, 189–91

Wound response
plant responses to insect herbivory and, 299–301, 308–12, 313

***WUS* gene**
Arabidopsis meristem maintenance and, 53, 56–61

X

***Xa* genes**
rice as comparative genomics model and, 410

Xanthogaleruca luteola
plant responses to insect herbivory and, 306

Xanthomonas oryzae
rice as comparative genomics model and, 409

Xenopus laevis
marine diatoms and, 113
nonselective cation channels and, 89, 93

X-ray crystallography
primary photochemistry of photosystem II and, 551–71
Rubisco and, 449–65

Xylogenesis
vascular tissue differentiation and pattern formation, 183–97

Y

***yabby* mutant**
vascular tissue differentiation and pattern formation, 195–96

***ycf1* mutant**
phytochelatins and metallothioneins, 163, 167

Yeast
auxin signaling and, 380–81

α -ketoacid dehydrogenase complexes and, 362, 368–69

marine diatoms and, 124

nonselective cation channels and, 86, 90–91, 94–95

phytochelatins and metallothioneins, 161–65, 167–69, 174, 177–78

phytochrome-dependent signaling and, 332, 340

regulation of lysine metabolism in plants and, 30

salt and drought stress signal transduction, 260

targeted mutagenesis in *Physcomitrella patens* and, 477

Z

***ZAG1* gene**
rice as comparative genomics model and, 408

Zea mays
chlororespiration and, 528
 α -ketoacid dehydrogenase complexes and, 368–69
lipoxygenase pathway and, 282–84
nonselective cation channels and, 75
root gravitropism and, 428–29

***Zinnia* spp.**
vascular tissue differentiation and pattern formation, 186, 197

***ZRR* gene**
nitrate signaling pathways and, 215

***ZTL/ADO/LKP* gene group**
phytochrome-dependent signaling and, 342

CONTENTS

Frontispiece—A. A. Benson	xii
PAVING THE PATH, <i>A. A. Benson</i>	1
NEW INSIGHTS INTO THE REGULATION AND FUNCTIONAL SIGNIFICANCE OF LYSINE METABOLISM IN PLANTS, <i>Gad Galili</i>	27
SHOOT AND FLORAL MERISTEM MAINTENANCE IN ARABIDOPSIS, <i>Jennifer C. Fletcher</i>	45
NONSELECTIVE CATION CHANNELS IN PLANTS, <i>Vadim Demidchik, Romola Jane Davenport, and Mark Tester</i>	67
REVEALING THE MOLECULAR SECRETS OF MARINE DIATOMS, <i>Angela Falciatore and Chris Bowler</i>	109
ABSCISSION, DEHISCENCE, AND OTHER CELL SEPARATION PROCESSES, <i>Jeremy A. Roberts, Katherine A. Elliott, and Zinnia H. Gonzalez-Carranza</i>	131
PHYTOCHELATINS AND METALLOTHIONEINS: ROLES IN HEAVY METAL DETOXIFICATION AND HOMEOSTASIS, <i>Christopher Cobbett and Peter Goldsbrough</i>	159
VASCULAR TISSUE DIFFERENTIATION AND PATTERN FORMATION IN PLANTS, <i>Zheng-Hua Ye</i>	183
LOCAL AND LONG-RANGE SIGNALING PATHWAYS REGULATING PLANT RESPONSES TO NITRATE, <i>Brian G. Forde</i>	203
ACCLIMATIVE RESPONSE TO TEMPERATURE STRESS IN HIGHER PLANTS: APPROACHES OF GENE ENGINEERING FOR TEMPERATURE TOLERANCE, <i>Koh Iba</i>	225
SALT AND DROUGHT STRESS SIGNAL TRANDUCTION IN PLANTS, <i>Jian-Kang Zhu</i>	247
THE LIPOXYGENASE PATHWAY, <i>Ivo Feussner and Claus Wasternack</i>	275
PLANT RESPONSES TO INSECT HERBIVORY: THE EMERGING MOLECULAR ANALYSIS, <i>André Kessler and Ian T. Baldwin</i>	299
PHYTOCHROMES CONTROL PHOTOMORPHOGENESIS BY DIFFERENTIALLY REGULATED, INTERACTING SIGNALING PATHWAYS IN HIGHER PLANTS, <i>Ferenc Nagy and Eberhard Schäfer</i>	329

THE COMPLEX FATE OF α -KETOACIDS, <i>Brian P. Mooney, Jan A. Miernyk, and Douglas D. Randall</i>	357
MOLECULAR GENETICS OF AUXIN SIGNALING, <i>Ottoline Leyser</i>	377
RICE AS A MODEL FOR COMPARATIVE GENOMICS OF PLANTS, <i>Ko Shimamoto and Junko Kyozuka</i>	399
ROOT GRAVITROPISM: AN EXPERIMENTAL TOOL TO INVESTIGATE BASIC CELLULAR AND MOLECULAR PROCESSES UNDERLYING MECHANOSENSING AND SIGNAL TRANSMISSION IN PLANTS, <i>K. Boonsirichai, C. Guan, R. Chen, and P. H. Masson</i>	421
RUBISCO: STRUCTURE, REGULATORY INTERACTIONS, AND POSSIBILITIES FOR A BETTER ENZYME, <i>Robert J. Spreitzer and Michael E. Salvucci</i>	449
A NEW MOSS GENETICS: TARGETED MUTAGENESIS IN <i>PHYSCOMITRELLA PATENS</i> , <i>Didier G. Schaefer</i>	477
COMPLEX EVOLUTION OF PHOTOSYNTHESIS, <i>Jin Xiong and Carl E. Bauer</i>	503
CHLORORESPARATION, <i>Gilles Peltier and Laurent Cournac</i>	523
STRUCTURE, DYNAMICS, AND ENERGETICS OF THE PRIMARY PHOTOCHEMISTRY OF PHOTOSYSTEM II OF OXYGENIC PHOTOSYNTHESIS, <i>Bruce A. Diner and Fabrice Rappaport</i>	551
INDEXES	
Subject Index	581
Cumulative Index of Contributing Authors, Volumes 43–53	611
Cumulative Index of Chapter Titles, Volumes 43–53	616
ERRATA	
An online log of corrections to <i>Annual Review of Plant Biology</i> chapters (if any, 1997 to the present) may be found at http://plant.annualreviews.org/	